

IN THE CLAIMS

Claims 1 – 22 (cancelled).

23. (new) A method of identifying a virus comprising:

amplifying nucleic acid from said virus with a pair of primers which hybridize to conserved regions of a housekeeping gene that is conserved among members of a viral family to produce an amplification product, wherein the amplification product corresponds to a bioagent identifying amplicon, and wherein the conserved regions have at least 80% sequence identity among members of said viral family which flank an intervening variable region which exhibits no greater than 5% sequence identity among members of said viral family;

measuring the molecular mass of said amplification product; and

comparing the molecular mass of said amplification product with known molecular masses of known bioagent identifying amplicons of members of said viral family wherein a match of molecular mass of said amplification product with a known mass of a known bioagent identifying amplicon of a member of said viral family indicates the identity of said virus.

24. (new) The method of Claim 23, further comprising repeating said amplifying, measuring and comparing steps using one or more additional pairs of primers.

25. (new) The method of Claim 23, wherein said virus is a biological warfare viral threat agent.

26. (new) The method of claim 23, wherein said virus is identified at the sub-species level.

27. (new) The method of Claim 23, wherein said molecular mass of said amplification product is measured by mass spectrometry.

28. (new) The method of Claim 23, wherein said pair of primers comprises at least one universal nucleobase.
29. (new) The method of Claim 28, wherein said universal nucleobase is inosine.
30. (new) A method of identifying a virus comprising:
amplifying nucleic acid from said virus with a pair of primers which hybridize to conserved regions of a housekeeping gene that is conserved among members of a viral family to produce an amplification product, wherein the amplification product corresponds to a bioagent identifying amplicon, and wherein the conserved regions have at least 80% sequence identity among members of said viral family which flank an intervening variable region which exhibits no greater than 5% sequence identity among members of said viral family;
measuring the base composition of said amplification product; and
comparing the base composition of said amplification product with known base compositions of known bioagent identifying amplicons of members of said viral family wherein a match of base composition of said amplification product with a known base composition of a known bioagent identifying amplicon of a member of said viral family indicates the identity of said virus.
31. (new) The method of Claim 30, further comprising repeating said amplifying, measuring and comparing steps using one or more additional pairs of primers.
32. (new) The method of Claim 30, wherein said virus is a biological warfare viral threat agent.
33. (new) The method of Claim 30, wherein said virus is identified at the sub-species level.

34. (new) The method of Claim 30, wherein said base composition of said amplification product is measured by mass spectrometry.
35. (new) The method of Claim 30, wherein said pair of primers comprises at least one universal nucleobase.
36. (new) The method of Claim 35, wherein said universal nucleobase is inosine.
37. (new) A method of identifying a virus belonging to a viral family comprising:
amplifying nucleic acid from said virus with a pair of primers which hybridize to conserved regions of a housekeeping gene that is conserved among members of a viral family to produce an amplification product, wherein the amplification product corresponds to a bioagent identifying amplicon that is about 45 to about 150 nucleobases in length having said conserved regions flanking a variable region;
measuring the molecular mass or base composition of said amplification product;
and
comparing the molecular mass or base composition of said amplification product with known molecular masses or base compositions of known bioagent identifying amplicons of members of said viral family wherein a match of molecular mass or base composition of said amplification product with a known molecular mass or base composition of a known bioagent identifying amplicon of a member of said viral family indicates the identity of said virus.
38. (new) The method of Claim 37, further comprising repeating said amplifying, measuring and comparing steps using one or more additional pairs of primers.
39. (new) The method of Claim 37, wherein said virus is a biological warfare viral threat agent.

40. (new) The method of Claim 37, wherein said virus is identified at the sub-species level.

41. (new) The method of Claim 37, wherein said molecular mass or base composition of said amplification product is measured by mass spectrometry.

42. (new) The method of Claim 37, wherein said pair of primers comprises at least one universal nucleobase.

43. (new) The method of Claim 42, wherein said universal nucleobase is inosine.